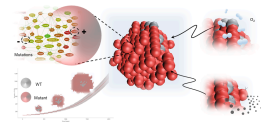


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## microC-protocol

DOI

[dx.doi.org/10.17504/protocols.io.vxue7nw](https://dx.doi.org/10.17504/protocols.io.vxue7nw)



Dimitrios Voukantsis<sup>1</sup>, Kenneth Kahn<sup>2</sup>, Martin Hadley<sup>2</sup>, Rowan Wilson<sup>2</sup>, Francesca M Buffa<sup>1</sup>

<sup>1</sup>Computational Biology and Integrative Genomics, MRC/CRUK Oxford Institute, University of Oxford, Oxford, Oxfordshire, OX3 7DQ, UK;

<sup>2</sup>Academic Information Technology Research Team, University of Oxford, Oxford, Oxfordshire, OX2 6NN, UK



Dimitrios Voukantsis

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External link: <http://microc.org>

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**Protocol status:** Working

**We use this protocol and it's working**

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**Keywords:** signalling networks, gene networks, molecular pathways, genotype to phenotype, agent-based modelling, microenvironment, executable biology, multiscale virtual microenvironment for perturbation biology, protocol microc, experiment with microc, multiscale virtual microenvironment, microc, gene network modelling, surrounding microenvironment, interactions among cell, perturbation biology, easy access to advanced computational modelling, genotype, simulation, phenotype, gene, advanced computational modelling, cell, wide variety of experiment, experiment

## Abstract

microC is a multiscale virtual microenvironment for perturbation biology. It enables experiments that link genotype to phenotype taking into account the surrounding microenvironment. microC has a modular architecture that enables a wide variety of experiment. Furthermore, it offers easy access to advanced computational modelling and supercomputing resources to the wider scientific community.

microC combines agent-based and gene network modelling and uses partial differential equations to simulate interactions among cells.

The tool itself does not require any installation on the user's machine, as it can be accessed using a web browser. Experimental results and data are also available via a web interface. This protocol describes the process of preparing and submitting an experiment with microC, and interpreting the simulation results

## Troubleshooting

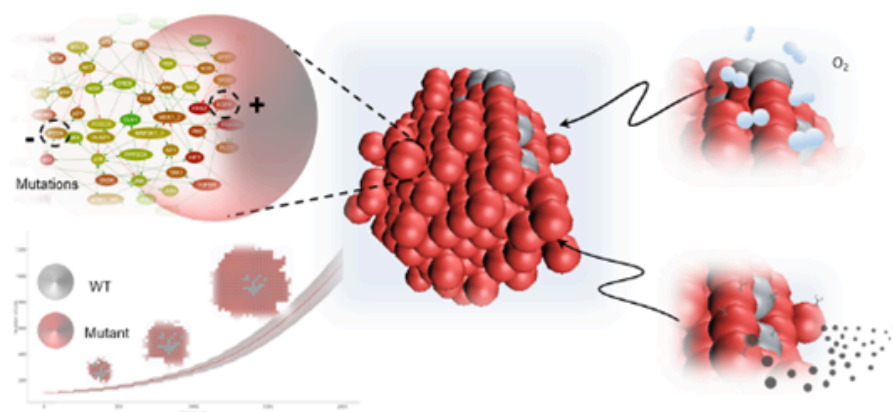
## Accessing microC

- 1 microC is available via [microc.org](http://microc.org). During the first visit this step might take several seconds. This will not be the case in future visits.

## Preparing an experiment

- 2 Experiments are specified via the microC main web page (Figure 1). The user may set a number of numerical parameters via sliders, specify the gene network, mutations, and parameters that control diffusion (please refer to the documentation page of microC for details, <http://microc.org>). microC modules are enabled through the specification files. For example setting parameters for *Oxygen* or any output node within diffusion-parameters.txt, will automatically enable a diffusion module for this substance. The "Run experiment" button submits the experiment to the computing cluster.

## Run virtual experiments with microC



Set the following sliders and buttons to specify the parameters of your experiment. See [the documentation](#).

Number of replicates: **48**

Cell Diameter: **100  $\mu\text{m}$**

Maximum number of simulation steps: **100**

Maximum number of cells: **500**

Initial number of cells: **100**

Cell decision window (# steps): **100**

Network update rate: **1**

Diffusion update rate: **1**

Grid sparsity: **1**

- ☐ Check this if you wish to run the model with a three dimensional array of cells.
- Use this to upload any customisations of the default settings. Any of mutations.txt, input.txt, or regulatoryGraph.html.

No file chosen

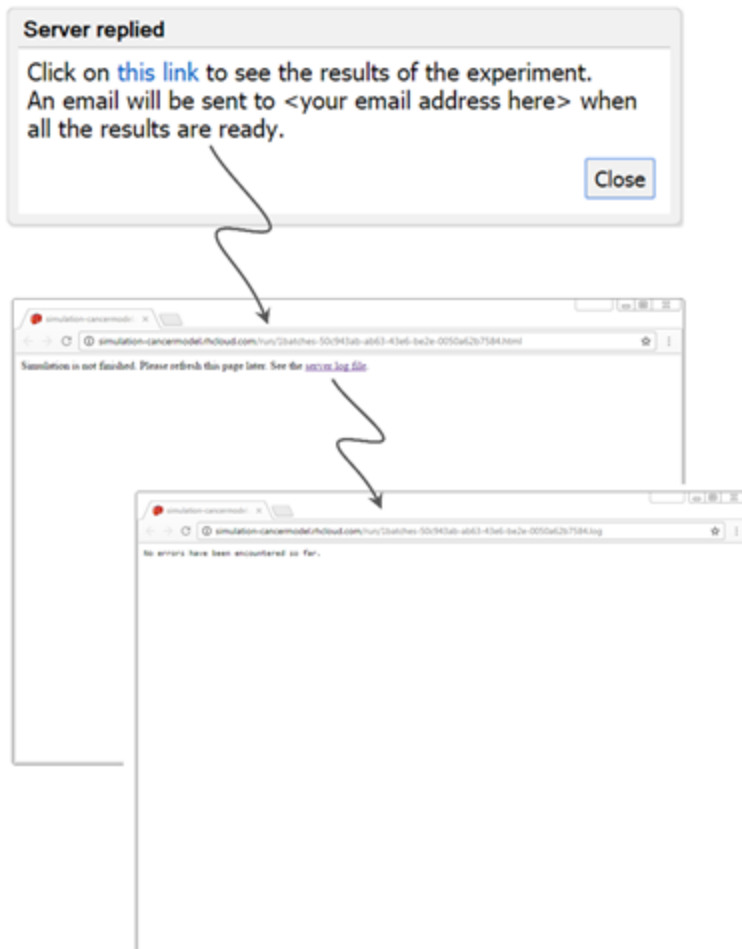
If you wish to be notified when the results are ready please enter your email:

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**Figure 1. microC main Interface.** Sliders are used to setup the numerical parameters, whereas the “Choose File” button may be used to upload local files that define the experiment. The check box enables switching between 2D/3D simulating environment. Finally, the “Run experiment” button submits the experiment.

## Submitting an experiment

- 3 Upon submission of the experiment ("Run Experiment" button, Figure 1) the user receives a link (Figure 2) that provides information about the status of the submission and the log file, where potential errors are shown. Once the experiment has finished the same link will contain the results (that gradually become available in batches 16 replicates). Optionally, the user will be notified by email.



**Figure 2.** Upon submission the user receives a confirmation and a link that will contain the results when the simulations will be finished.

## Evaluating the results

- 4 The results page displays data across all replicates and permits the viewer to inspect any of the replicates in detail. An animation of all replicates is displayed in the initial page along with averaged and detailed data for each of the experimental replicate (Figure 3). A more detailed presentation of the results page is available in the documentation page of microc (<http://microc.org>).

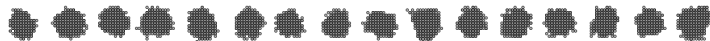
## 16 out of 16 results from running microC

Submitted at 2017-04-23 00:23

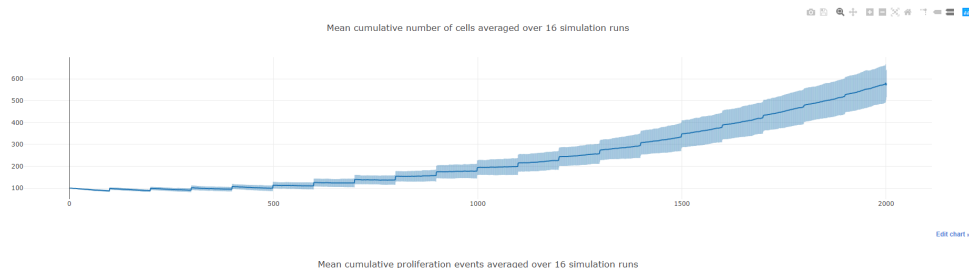
See [the general settings](#). See [the mutation settings](#). See [other settings](#).

### Animation of cells

To inspect an experimental replicate click on it.



### Averaged simulations results



**Figure 3. microC results overview.** Results are displayed as animations, along with graphs on cell populations and cell decisions. More detailed information on specific replicates are available on clicking the specific icon.